

**Supplementary Table S2. Statistical analysis of sheep testicular cells by Cell Ranger software**

<b>Sample</b>	<b>Testis</b>
Estimated Number of Cells	12,843
Mean Reads per Cell	38,730
Median Genes per Cell	1,338
Number of Reads	497,413,101
Valid Barcodes	97.90%
Sequencing Saturation	60.4%
Q30 Bases in Barcode	96.1%
Q30 Bases in RNA Read	92.8%
Q30 Bases in UMI	95.8%
Reads Mapped to Genome	92.9%
Reads Mapped Confidently to Genome	84.5%
Reads Mapped Confidently to Intergenic Regions	13.1%
Reads Mapped Confidently to Intronic Regions	16.2%
Reads Mapped Confidently to Exonic Regions	55.1%
Reads Mapped Confidently to Transcriptome	51.5%
Reads Mapped Antisense to Gene	1.0%
Fraction Reads in Cells	63.5%
Total Genes Detected	22,033
Median UMI Counts per Cell	2,759